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       Evans, Cheryl
       Merberg, David
       Treacy, Maurice
       Bowman, Michael R.
       Spaulding, Vikki
       Agostino, Michael J.
       Genetics Institute, Inc.
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- Cys Lys Leu His Ala Leu Phe Thr Leu Ala Gln Ala Glu Asp Ser Val 35 40 45
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- Val Lys Leu Pro Lys Ser Ser Ser Gln Glu Val Glu Ala Lys Glu Leu 65 70 75 80
- Ser Phe Val Leu Asp Tyr Ile Asn Gln Ser Pro Lys Cys Ile Ala Phe 85 90 95
- Gly Asn Glu Gly Val Tyr Val Ala Ala Val Arg Glu Phe Tyr Leu Ser 100 105 110
- Val Tyr Phe Phe Lys Lys Lys Thr Thr Ser Arg Phe Thr Leu Ser Ser 115 120 125
- Ser Arg Asn Lys Lys His Ala Lys Asn Asn Phe Thr Cys Val Ala Cys 130 135 140
- His Pro Thr Glu Asp Cys Ile Ala Ser Gly His Met Asp Gly Lys Ile 145 150 155 160
- Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr Tyr Thr Cys
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- Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe Ser Val Thr 180 185 190
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- Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg Leu Gly Ala 210 215 220
- Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu Phe Cys Thr 225 230 235 240
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- Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile Phe Thr Gly 260 265 270
- Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn Gly Lys Pro 275 280 285
- Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln Leu Tyr Asn 290 295 300
- Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly Leu Ile Gln 305 310 315 320

Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn Trp Leu Ala 325 330 335

- Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu Leu Gln Met 340 345 350
- Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile Leu Asn Thr 355 360 365
- Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu Cys Phe Cys 370 380
- Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala Ser Lys Asp 385 390 395 400
- Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp Ile Tyr Lys
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- Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr His Lys Tyr 420 425 430
- Gln Ala Thr Asn Cys Cys Phe Ser Glu Asp Gly Ser Leu Leu Ala Val 435 440 445
- Ser Phe Glu Glu Ile Val Thr Ile Trp Asp Ser Val Thr Trp Glu Leu 450 455 460
- Lys Cys Thr Phe Cys Gln Arg Ala Gly Lys Ile Arg His Leu Cys Phe 465 470 475 480
- Gly Arg Leu Thr Cys Ser Lys Tyr Leu Leu Gly Ala Thr Glu Asn Gly
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- Lys Leu Asn Val Arg Val Met Glu Pro Asp Pro Asn Ser Glu Asn Ile 515 520 525
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- Pro Ser Glu Pro Arg Pro Leu Tyr Ile Gln Lys Gly Ile Ser Arg Glu 545 550 555 560
- Lys Val Gln Trp Gly Val Phe Val Pro Arg Asp Val Pro Glu Ser Phe 565 570 575
- Thr Ser Glu Ala Tyr Gln Trp Leu Asn Arg Ser Gln Phe Tyr Phe Leu 580 585 590
- Thr Lys Ser Gln Ser Leu Leu Thr Phe Ser Thr Lys Ser Pro Glu Glu
 595 600 605
- Lys Leu Thr Pro Thr Ser Lys Gln Leu Leu Ala Glu Glu Ser Leu Pro 610 620
- Thr Thr Pro Phe Tyr Phe Ile Leu Gly Lys His Arg Gln Gln Gln Asp 625 630 635 640

Glu Lys Leu Asn Glu Thr Leu Glu Asn Glu Leu Val Gln Leu Pro Leu 645 650 655

Thr Glu Asn Ile Pro Ala Ile Ser Glu Leu Leu His Thr Pro Ala His 660 665 670

Val Leu Pro Ser Ala Ala Phe Leu Cys Ser Met Phe Val Asn Ser Leu 675 680 685

Leu Leu Ser Lys Glu Thr Lys Ser Ala Lys Glu Ile Pro Glu Asp Val 690 695 700

Asp Met Glu Glu Glu Lys Glu Ser Glu Asp Ser Asp Glu Glu Asn Asp 705 710 715 720

Phe Thr Glu Lys Val Gln Asp Thr Ser Asn Thr Gly Leu Gly Glu Asp 725 730 735

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 Arg Leu Thr Leu Arg Asp Leu Gln Asn Lys Ser Ser Ser Cys Ser Ser
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Pro Ser Ser Ser Ala Thr Ser Leu Leu His Thr Val Ser Pro Glu Pro
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Pro Arg Pro Pro Gln Gln Pro Val Pro Thr Glu Leu Ser Leu Ala Ser
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Ile Thr Val Pro Leu Glu Ser Ile Lys Pro Ser Asn Ile Leu Pro Val
            100
                               105
Thr Val Tyr Asp Gln His Gly Phe Arg Ile Leu Phe His Phe Ala Arg
Asp Pro Leu Pro Gly Arg Ser Asp Val Leu Val Val Val Ser Met
                       135
Leu Ser Thr Ala Pro Gln Pro Ile Arg Asn Ile Val Phe Gln Ser Ala
145
                                       155
Val Pro Lys Val Met Lys Val Lys Leu Gln Pro Pro Ser Gly Thr Glu
               165
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Cys Gln Glu Tyr Leu Asn Gln Cys Cys His Phe Xaa Leu Glu Asp Met
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Leu Tyr Ala Ala Ser Ser Ile Lys Ser Asn Tyr Leu Val Phe Met Ala
                              40
Glu Leu Phe Trp Trp Phe Glu Val Val Lys Pro Ser Phe Val Gln Pro
Arg Val Val Arg Pro Gln Gly Ala Glu Pro Val Lys Asp Met Pro Ser
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Ile Pro Val Leu Asn Ala Ala Lys Arg Asn Val Leu Asp Ser Ser Ser
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  agecectatg atggagacet caccamtace tectecteec tetteatega cagecteace 180
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 Pro Tyr Asp Gly Asp Leu Thr Xaa Thr Ser Ser Ser Leu Phe Ile Asp
                             40
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Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val
His Leu Gly Thr Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala
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Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu 195 200 205

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Ser Asp Leu Ile Tyr Lys Leu Tyr Val Val Gln Thr Val Ile Lys Thr
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Ala Lys Phe Ile Phe Ile Leu Cys Tyr Thr Ala Asn Phe Val Asn Ala
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Ile Ser Phe Glu His Val Cys Lys Pro Lys Val Glu His Leu Ile Gly
Tyr Glu Val Phe Glu Cys Thr His Asn Met Ala Tyr Met Leu Lys Lys
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- Phe Glu Lys Val Arg Glu Glu Ser Ser Phe Ser Asp Ile Pro Asp Val 145 150 155 160
- Lys Asn Asp Phe Ala Phe Leu Leu His Met Val Asp Gln Tyr Asp Gln 165 170 175
- Leu Tyr Ser Lys Arg Phe Gly Val Phe Leu Ser Glu Val Ser Glu Asn 180 185 190
- Lys Leu Arg Glu Ile Ser Leu Asn His Glu Trp Thr Phe Glu Lys Leu 195 200 205
- Arg Gln His Ile Ser Arg Asn Ala Gln Asp Lys Gln Glu Leu His Leu 210 215 220
- Phe Met Leu Ser Gly Val Pro Asp Ala Val Phe Asp Leu Thr Asp Leu 225 230 230 240
- Asp Val Leu Lys Leu Glu Leu Ile Pro Glu Ala Lys Ile Pro Ala Lys 245 250 255
- Ile Ser Gln Met Thr Asn Leu Gln Glu Leu His Leu Cys His Cys Pro 260 265 270
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- Cys Leu His Val Lys Phe Thr Asp Val Ala Glu Ile Pro Ala Trp Val
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- Ser Glu Asn Asn Lys Met Ile Gly Leu Glu Ser Leu Arg Glu Leu Arg 325 330 335
- His Leu Lys Ile Leu His Val Lys Ser Asn Leu Thr Lys Val Pro Ser 340 345 350
- Asn Ile Thr Asp Val Ala Pro His Leu Thr Lys Leu Val Ile His Asn 355 360 365
- Asp Gly Thr Lys Leu Leu Val Leu Asn Ser Leu Lys Lys Met Met Asn 370 375 380
- Val Ala Glu Leu Glu Leu Gln Asn Cys Glu Leu Glu Arg Ile Pro His 385 390 395 400
- Ala Ile Phe Ser Leu Ser Asn Leu Gln Glu Leu Asp Leu Lys Ser Asn 405 410 415
- Asn Ile Arg Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu Lys Arg
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 Cys Leu Asp Val Ser Tyr Asn Asn Ile Ser Met Ile Pro Ile Glu Ile
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Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro
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Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val Pro
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Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Pro Leu Glu Ala
Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro
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Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile
        115
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Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu
                        135
Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr
145
                   150
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Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
485 490 495

Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
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Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe 515 520 525

Arg Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser 530 535 540

Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe 545 550 555 560

Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp 565 570 575

Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile 580 585 590

Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
595 600 605

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Ile Gly Ile Gly Glu Leu Ile Thr Arg Ser Xaa Lys His Ile Phe Lys
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Thr Tyr Leu Gln Gly Val Glu Leu Ser Gly Leu Ser Ala Ala Ile Ser
His Phe Leu Asn Cys Phe Leu Ser Ser Tyr Pro Asn Pro Val Ala His
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Leu Pro Ala Asp Glu Leu Val Ser Lys Lys Arg Asn Lys Arg Arg Lys
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Pro Glu Arg Lys Asn Gln Glu Lys Glu Ser Asp Asp Ala Leu Thr Val
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Asn Glu Glu Thr Ser Glu Glu Asn Asn Gln Met Glu Glu Ser Asp Val
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Ser Gln Ala Glu Lys Asp Leu Leu His Ser Glu Gly Ser Glu Asn Glu
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Gly Pro Val Ser Ser Ser Ser Asp Cys Arg Glu Thr Glu Glu Leu
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PCT/US00/25135 WO 01/19988

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Gly Leu Leu Gln Ser Tyr Leu Lys Gly Leu Gly Arg Thr Glu Val Gln
Leu Glu His Leu Ser Arg Glu Gln Val Leu Leu Tyr Leu Phe Ala Leu
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                                        75
His Asp Tyr Asp Gln Ser Gly Gln Leu Asp Gly Leu Glu Leu Leu Ser
Met Leu Thr Ala Ala Leu Ala Pro Gly Ala Ala Asn Ser Pro Thr Thr
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Asn Pro Val Ile Leu Ile Val
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Lys Glu His Glu Lys Glu Gly Glu Asp Gly Tyr Gly Lys Leu Gly Arg
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Gln Asp Gly Asp Glu Glu Phe Glu Glu Glu Glu Glu Glu Ser Glu Asn
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Lys Ser Met Asp Thr Asp Pro Glu Thr Ile Arg Asp Glu Glu Glu Thr
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105

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- Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys 50 55 60
- Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val 65 70 75 80
- Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro 85 90 95
- Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu 100 105 110
- Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu 115 120 125
- Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser 130 135 140
- Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys 145 150 155 160
- Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala 165 170 175
- Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile 180 185 190
- Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile 195 200 205
- Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro 210 215 220
- Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp 225 230 235 240
- Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile 245 250 255
- Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys 260 265 270
- Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr 275 280 285
- Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val 290 295 300
- Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu 305 310 315 320
- Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr 325 330 335

Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp 340 345 350

Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr 355 360 365

Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr 370 375 380

Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr 385 390 395 400

Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu 405 410 415

Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro 420 425 430

Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp 435 440 - 445

Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys 450 455 460

Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly 465 470 475 480

Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu 485 490 495

Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu 500 505 510

Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu 515 520 525

Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg 530 535 540

Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser 545 550 555 560

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Ser Pro Tyr 595

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ctgtgttcca gctgacagac gtgCtaatta tcctgttttc tgtgtccaga caaaqactac 300
aagaatttca acagtaacag caacaacagc aacaacaact ttgatgatga ctactgcttc 360
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Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Leu Met Met Thr Thr
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Glu Glu Glu Arg

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Leu Ala Leu Arg Ala Asp Tyr Glu Ile Ala Ser Lys Glu Arg Asp Leu 65 70 75 80

Phe Phe Glu Leu Asp Ala Met Asp His Leu Glu Ser Phe Ile Ala Glu

85 90 95

Cys Asp Arg Arg Thr Glu Leu Ala Lys Lys Arg Leu Ala Glu Thr Gln
100 105 110

Glu Glu Ile Ser Ala Glu Val Ser Ala Lys Ala Gly Lys Val His Glu 115 120 125

Leu Asn Glu Glu Ile Gly Lys Leu Leu Ala Lys Ala Glu Gln Leu Gly 130 135 140

Lys Val Arg Ala Lys Lys Glu Ala Glu Glu Glu Tyr Arg Asn Ser 165 170 175

Met Pro Ala Ser Ser Phe Gln Gln Lys Leu Arg Val Cys Glu Val 180 185 190

Cys Ser Ala Tyr Leu Gly Leu His Asp Asn Asp Arg Arg Leu Ala Asp 195 200 205

His Phe Gly Gly Lys Leu His Leu Gly Phe Ile Gln Ile Arg Glu Lys 210 215 220

Leu Asp Gln Leu Arg Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn 225 230 235 240

Gln Asp Arg Leu Arg Arg Glu Glu Arg Glu Glu Arg Leu 245 250 255

Ser Arg Arg Ser Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser 260 265 270

Arg Asp Arg Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg 275 280 285

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Ser Ala Lys Tyr Lys 325

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Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp Glu Asn Glu
                            40
Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr Pro Val Ser Gly
                        55
Glu Glu Gly Arg Ala Ala Pro Asp Val Ala Pro Ala Pro Gly Pro
                    70
                                       75
Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly Met Leu Arg Lys Leu Phe
Ser Ser His Arg Phe Gln Val Ile Ile Ile Cys Leu Val Val Leu Asp
           100
Ala Leu Leu Val Leu Ala Glu Leu Ile Leu Asp Leu Lys Ile Ile Gln
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                           120
Pro Asp Lys Asn Asn Tyr Ala Ala Met Val Phe His Tyr Met Ser Ile
Thr Ile Leu Val Phe Phe Met Met Glu Ile Ile Phe Lys Leu Phe Val
145
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Val Val Val Val Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu
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His Gln Phe Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg
        195
                             200
Val Ala Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser
                         215
Glu Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala
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                    230
                                         235
Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Glu Gln Glu Ile
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Ile Arg Arg Lys
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Val Ser Leu Lys His Phe Pro Thr Lys Lys Leu Lys Thr His Val Leu 50 55 60

Glu Thr His Ala Tyr Val Ser Leu Ile Ile Leu Asn Ile Phe Lys Met 65 70 75 80

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Ile Phe Trp Ile Asn
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Ser Lys Pro Val
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acctetecta gateteagaa atgeetagaa agagaagtee tggetacate aatggaaatt 240
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attatettea ttagtatate teaattttgt caatacaaac etgagagtta tagteagagg 420
tigaattite atticaaaat giitteetag tittititet ettititigit tiatigtaag 480
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Lys Trp Lys Leu Val Phe Gln Val Gln Asn Lys Asn Lys Thr His Phe
        35
                           40
Phe Thr Cys Leu Lys Met Cys Thr
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aattttccta ttccaatacc tgaatctgcc cctacaactc cccttcctag cgaaaagtaa 300
acaagaagga aaagtcacga taaacctggt cacctgaaat tgaaattgag ccacttcctt 360
gaagaatcaa aattootgtt aataaaagaa aaacaaatgt aattgaaata gcacacagca 420
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aaaaaaaaaa aaaaaaaaa aaaaaaaaaa aaaaa
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Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
                             40
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
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                                         75
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tettteanae aacattette ttaacattge tgteettgag gaettaeean antgaagtet 240
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accoaggatg tgcctcggtg atttccagtg gaagaatgta ggtcccaata ccacaagcac 300
agtcattage acagatgett ttaggecagg agttegatat gactteagaa tttatgggtt 360
atctacaaaa aggattgctt gtttattaga gaaaaaaaac aggatactct caggaacttg 420
cteetteaga caacceteac gigetggtgg atacattgac atcceactee tteactetga 480
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56

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Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His
         35
                              40
Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys
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ccattcacta gtgctggtga aggccccagt gcnacgttca cgaaggtcac gactccggat 180
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PCT/US00/25135 WO 01/19988

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tgccaatgga aagateetgt tetataatgt agttgtagaa aacetagaca aaceateeag 180
ttcagagete cattecatte cageaceage caacageaca aaactaatee ttgacaggtg 240
ttcctaccaa atctgcgtca tagccaacaa cagtgtgggt gcttctcctg cttctgtaat 300
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gaatttatgg gttatctaca aaaaggattg cttgtttatt agagaaaaaa aacaggatac 600
teteaggaae ttgeteette agacaaeeet caegtgetgg tggatacatt gacateeeae 660
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<210> 91
<211> 58
<212> PRT
<213> Homo sapiens
<400> 91
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Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His
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Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys
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<210> 92
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<212> DNA
<213> Homo sapiens
<400> 92
aaaaaaaaa aaaaaaaaa
<210> 93
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<211> 1939
<212> DNA
<213> Homo sapiens
<400> 93
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<213> Homo sapiens
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             20
                                25
Ser Trp Ser Val Gly Leu Ser Pro Leu Leu Ile Phe Ser Glu Asn His
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Phe Leu Phe Leu
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59

<212> DNA <213> Homo sapiens

<400> 95

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<210> 96

<211> 289

<212> PRT

<213> Homo sapiens

<400> 96

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Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp Cys Gly Ser Thr Asp 35 40 45

Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu Thr Asp Ser Val Leu 50 60

Glu Thr Met Gly Arg Val Ser Leu Asp Met Met Ser Val Gln Ala Asn 65 70 75 80

Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr Ala Val Trp Arg Gly 85 90 95

Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val Lys Leu Ser Arg Lys
100 105 110

His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn Phe Phe Phe Lys 115 120 125

His Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe 130 135 140

Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala

155

160

150

145

Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys 165 170 Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp 180 185 Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu Lys 200 Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile Ala Lys 215 Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp Asp Ile Phe 230 235 Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn Leu Gln Val Ser 245 250 Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg Lys Lys Thr Lys Asp Glu 280 Leu <210> 97 <211> 492 <212> DNA <213> Homo sapiens <400> 97 ctaggttctg ggaagatggc gaaggtctca gagctttacg atgtcacttg ggaagaaatg 60 agagataaaa tgagaaaatg gagagaagaa aactcaagaa atagtgagca aattgtggaa 120 gttggagaag aattaattaa tgaatatgct tctaagctgg gagatgatat ttggatcata 180 tatgaacagg tgatgattgc agcactagac tatggtcggg atgacttggc attgttttgt 240 cttcaagagc tgagaagaca gttccctggc agtcacagag tcaagcgatt aacaggcatg 300 agatttgaag ccatggaaag atatgatgat gctatacagc tatatgatag gattttacaa 360 gaagatccaa ctaacactgc tgcaagaaag cgtaagattg ccattcgaaa agcccagggg 420 aaaaatgtgg aggccattcg ggagctgaat gagtatctgg aacaatttgt tggagaccaa 480 gaagcctggc at 492 <210> 98 <211> 159 <212> PRT <213> Homo sapiens <400> 98 Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met Arg Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn Ser Glu Gln 20 25 Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys Leu 35 40 45

Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala Leu 55 50 Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp Arg 105 Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys Ile 120 125 Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu Leu 135 Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His - 155 <210> 99 <211> 85 <212> DNA <213> Homo sapiens <220> <221> unsure <222> (20) <220> <221> unsure <222> (27) <400> 99 ccttgttaaa taaaccatgn tgatttntta aacttgccaa aaaaaaaaaa aaaaaaaaa 60 aaaaaaaaa aaaaaaaaa aaaaa <210> 100 <211> 313 <212> DNA <213> Homo sapiens <220> <221> unsure <222> (68) <220> <221> unsure <222> (108) <220> <221> unsure <222> (137) <220> <221> unsure <222> (288)

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cttgtatcga catcattcaa aagctcttca aagcatttgt tcaaatcttc agtactggcc 240
agttttcata cagtctcggg gttttaaaac tttgaaatca aggacacnac gtctccagtc 300
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 Asp Ala Met Pro Ile Asn Lys Ala Thr Ile Met Pro Arg Gly Pro Thr
                          55
      50
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Phe Arg Asn Ser Thr Ala Thr Tyr Lys Ser Ser Leu Glu Leu Ser Gly
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Tyr Leu Lys Ser Glu Ala Ser Thr Phe Leu Arg Thr Lys His Arg Asn
Asp Glu Met Ser Tyr Lys Tyr Pro Phe Ile Leu Phe His Asn Thr Tyr
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tgentttgge ceeggeetgg ceaaaanage ceateceeag ggeagtttea ggtgeegget 240
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Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu 50 55 60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala 65 70 75 80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile 100 105 110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr 115 120 125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile 130 135 140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His 145 150 155 160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys 165 170 175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr 180 185 190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe 195 200 205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys 210 215 220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Gln Thr Ile Leu Pro Ser 225 230 235 240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
245 250 255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His 260 265 270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp 275 280 285

Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp 295 Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser 315 310 Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Cys Glu 330 325 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro 360 Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr 390 395 Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys 410 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly 420 425 Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro 440 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Gln Ala Leu 455 <210> 113 <211> 355 <212> DNA <213> Homo sapiens <220> <221> unsure <222> (133) <220> <221> unsure <222> (151) <220> <221> unsure <222> (196) <220> <221> unsure <222> (228) <400> 113 ctctcatttt tcctttcgaa gtgatatcca ctcgaacgag atcaaatctg taagctggag 60 atacaacttc cactacataa gatccagaag gtatatcatg aaccacaaaa ctcccatctg 120

tettaaggaa aengaegtge tetteteegt ntaccageae tegggeegee gagatecagt 180

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Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp
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Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys
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Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys Arg
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Ser Cys Leu Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn 50 55 60

Ile Leu Ile Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile 65 70 75 80

Pro Asp Leu Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val 85 90 95

Ala Asp Ser Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp 100 105 110

Ile Ala Val Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met
115 120 125

Tyr Ser Ser Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile 130 135 140

Ala Leu Ala Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His 145 150 155 160

Ala Arg Leu Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr 165 170 175

Leu Val Pro Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys 180 185 190

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            20
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Lys Glu Gln Cys Pro Tyr Thr Ser Glu Asp Glu Cys Ile Lys Asp Phe
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                                            60
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           100
Lys Arg Val Arg Leu Ala Lys Glu Gln Glu Ser Arg Ala Asp Cys Ile
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235

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230

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Thr	Phe	Ala	Cys	Val 325	Ser	Asp	Pro	Lys	Ala 330	Ala	Lys	Asp	Leu	Val 335	Leu
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GIn	Gln	T.eu	Ser	Asn	Asp	Gly	Met	Len	Va 1	Tle	Len	Δ1 a	Δla	Glv	Asn

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Thr Thr Ser Pro Leu Glu Cys Gly Phe Gly Gln Ser Val Thr Ser Val
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Lys Glu Gln Lys Asn Leu Glu Ser Ser Thr Gly Phe Gln Ile Pro Ser 130 135 140

Gln Glu Leu Ala Ser Gln Ile Asp Pro Gln Lys Asp Ile Glu Pro Arg 145 150 155 160

Thr Thr Tyr Gln Ile Glu Asn Phe Ala Gln Ala Phe Gly Ser Gln Phe 165 170 175

Lys Ser Gly Ser Arg Val Pro Met Thr Phe Ile Thr Asn Ser Asn Gly 180 185 190

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Ile Asp Ser Val Thr Ser Ser Gly Thr Ala Pro Ser Thr Thr Val Ser 50 55 60

Thr Ala Ala Thr Thr Pro Gly Ser Ala Ile Asp Thr Arg Glu Glu Leu 65 70 75 80

Val Asp Arg Val Phe Asp Glu Ser Leu Asn Phe Gln Lys Ile Pro Pro 85 90 95

Leu Val His Ser Lys Thr Pro Glu Gly Asn Asn Gly Arg Ser Gly Asp 100 105 110

Pro Arg Pro Gln Ala Ala Glu Pro Pro Asp His Leu Thr Ile Thr Arg 115 120 125

Arg Arg Thr Trp Ser Arg Asp Glu Val Met Gly Asp Asn Leu Leu Leu 130 135 140

Ser Ser Val Phe Gln Phe Ser Xaa Lys Ile Arg Gln Ser Ile Asp Lys 145 150 155 160

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Asp Asp Ile Glu Ser Lys Leu Arg Ala Glu Ser Glu Val Pro Ile Val 180 185 190

Lys Thr Ser Ser Met Glu Ile Ser Ser Ile Leu Gln Glu Leu Lys Arg 195 200 205

Val Glu Lys Gln Leu Gln Ala Ile Asn Ala Met Ile Asp Pro Asp Gly 210 215 220

Thr Leu Glu Ala Leu Asn Asn Met Gly Phe Pro Ser Ala Met Leu Pro 225 230 235 240

Ser Pro Pro Lys Gln Lys Ser Ser Pro Val Asn Asn His His Ser Pro 245 250 255

Gly Gln Thr Pro Thr Leu Gly Gln Pro Glu Ala Arg Ala Leu His Pro 260 265 270

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35 40 45 Tyr Asp Leu Leu Cys Leu Tyr Tyr His Glu Pro Val Ser Ser Asp Lys 55 Val Thr Xaa Lys Gln Phe Gln Leu Lys Glu Ile Val Leu Glu Leu Val 70 Ala His Val Leu Glu His Lys Ala Ile Gly Phe Val Met Val Asp Ala Lys Lys Glu Ala Lys Leu Ala Lys Leu Gly Phe Asp Glu Glu Gly 100 Ser Leu Tyr Ile Leu Lys Gly Asp Arg Thr Ile Glu Phe Asp Gly Glu 120 Phe Ala Ala Asp Val Leu Val Glu Phe Leu Leu Asp Leu Ile Glu Asp 130 135 140 Pro Val Glu Ile Ile Ser Ser Lys Leu Glu Val Gln Ala Phe Glu Arg 150 155 Ile Glu Asp Tyr Ile Lys Leu Ile Gly Phe Phe Lys Ser Glu Asp Ser 170 Glu Tyr Tyr Lys Ala Phe Glu Glu Ala Ala Glu His Phe Gln Pro Tyr 180 185 Ile Lys Phe Phe Ala Thr Phe Asp Lys Gly Val Ala Lys Lys Leu Ser 200 Leu Lys Met Asn Glu Val Asp Phe Tyr Glu Pro Phe Met Asp Glu Pro 210 Ile Ala Ile Pro Asn Lys Pro Tyr Thr Glu Glu Glu Leu Val Glu Phe 235 Val Lys Glu His Gln Arg Cys Leu Arg Trp His Val Gly Ala Gly Gly 245 250 Leu Gly Ser Gly Glu Trp Arg Gly Ala Ser Leu Cys 260 <210> 148 <211> 1009 <212> DNA <213> Homo sapiens <400> 148 gaattcggcc ttcatgcgcc tgcaggaaag aatctgacat catcacactg tgttttcctt 60 aacttgacag gaagtcaact tcaagcagat tgacttgaaa cgggatctca tttaggaagc 120 ataagtgtcc aatcaaaaac tgtgtatttt tttaaatttg gaaaatactc aagttccagt 180 tgcttateat teteetteae tttetgaaaa eetggeaate eeatgtggae ttetggtaga 240 atgageaatg caaagaactg gettggaett ggeatgteet tgtaettetg ggggetgatg 300 gaccttacga ccaccgttct ctcggacacc ccaacaccac aaggtgaatt agaagcactc 360 ctgtcagaca agccacagtc acatcagegg accaagarga getgggtttg gaaccagttt 420

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Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr 105

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Ile Pro Ile Gly Arg Leu His Leu Leu Pro Ser Ser Pro Ser
                       55
     50
Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Pro Ser Phe Ser
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Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
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Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
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gttgagagtc tgcgattatg aagagcagga tcttattact tcaatgaaag catgtaacaa 1140
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Trp Tyr His Val Val Gly Leu Ile Trp Ile Ser Glu Phe Ile Leu Ala
Cys Gln Gln Met Thr Val Ala Gly Ala Val Val Thr Tyr Tyr Phe Thr
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Arg Asp Lys Arg Asn Leu Pro Phe Thr Pro Ile Leu Ala Ser Val Asn
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Arg Leu Ile Arg Tyr His Leu Gly Thr Val Ala Lys Gly Ser Phe Ile
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Ile Thr Leu Val Lys Ile Pro Arg Met Ile Leu Met Tyr Ile His Ser
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Gln Leu Lys Gly Lys Glu Asn Ala Cys Ala Arg Cys Val Leu Lys Ser
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Cys Ile Cys Cys Leu Trp Cys Leu Glu Lys Cys Leu Asn Tyr Leu Asn
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Gln Asn Ala Tyr Thr Ala Thr Ala Ile Asn Ser Thr Asn Phe Cys Thr
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Ser Ala Lys Asp Ala Phe Val Ile Leu Val Glu Asn Ala Leu Arg Val
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Leu Ile Val Cys Ser Thr Gly Leu Ala Gly Ile Met Leu Leu Asn Tyr 195 200 205

Gln Gln Asp Tyr Thr Val Trp Val Leu Pro Leu Ile Ile Val Cys Leu 210 215 220

Phe Ala Phe Leu Val Ala His Cys Phe Leu Ser Ile Tyr Glu Met Val 225 230 235 240

Val Asp Val Leu Phe Xaa Xaa Phe Ala Ile Xaa Thr Lys Tyr Asn Asp 245 250 255

Gly Xaa Pro Gly Arg Glu Phe Tyr Met Asp Lys Val Leu Met Glu Phe 260 265 270

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Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg
Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu Lys Arg
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Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp
Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu
                               105
Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu
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Met Asp Gln Lys Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly
                        135
Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr
                                       155
145
                    150
Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu
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Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val
                               185
Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu
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200

195

235

Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val 210 215 220 Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp

Glu Lys Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly
245 250 255

230

Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala

Lys Leu Arg Leu Gln Ala.Gln Ser Leu Ser Thr Val Gly Pro Arg Leu 275 280 285

Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr 290 295 300

Lys Arg Arg Val Lys Lys Île Arg Lys Lys Glu Lys Glu Val Val 305 310 315 320

Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp 325 330 335

Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val 340 345 350

Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr 355 360 365

Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro 370 375 380

Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu 385 390 395 400

Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln
405 410 415

Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys 420 425 430

Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu
435 440 445

Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr 450 455 460

Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln 465 470 475 480

Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly
485 490 495

Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn 500 505 510

Leu Asp Glu Glu Lys Gln Gln Gln Asp Val Arg Ala Thr Pro Leu Gly 515 520 525

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122

35 40 45

Asn Pro Ser Leu Gln Thr Lys Ala Asn Leu Met Ser Ser Asn Ser Tyr 50 55 60

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Asn Leu Lys Asn Lys Gln Cys Ser Ile Ser Val His Ile Lys Gly Thr 85 90 95

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Gln Pro Phe Gln
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caggageete aaaagteaaa agggaaaaag aaaaaagaga aaaaaaagca ggaetttgat 300
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Lys Lys Gln Asp Phe Asp Glu Asp Asp Ile Leu Lys Glu Leu Glu Glu

60 55 50 Leu Ser Leu Glu Ala Gln Gly Ile Lys Ala Asp Arg Glu Thr Val Ala 75 Val Lys Pro Thr Glu Asn Asn Glu Glu Phe Thr Ser Lys Asp Lys Lys Lys Lys Gly Gln Lys Gly Lys Lys Gln Ser Phe Asp Asp Asn Asp 105 Ser Glu Glu Leu Glu Asp Lys Asp Ser Lys Ser Lys Thr Ala Lys 115 120 Pro Lys Val Glu Met Tyr Ser Gly Ser Asp Asp Asp Asp Phe Asn 135 Lys Leu Pro Lys Lys Ala Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys 150 155 145 Trp Asp Gly Ser Glu Glu Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu 170 Arg Ser Arg Ile Asn Ser Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu 185 Phe Leu Gln Ser Lys Arg Thr Glu Lys Lys Ser Glu Lys Gln Ala Arg 200 195 Ser <210> 183 <211> 912 <212> DNA <213> Homo sapiens <400> 183 ttactaagtt gatgttttct tttggtgaag ggcaatgtgg aatttaaatc atatagttca 120 tgtgtgcacc tgtcctgcag tttgaggcag atgattttaa accagcatct atagacactt 180 cctgtgaagg agagcttcaa gttggcaaag gagatgaagt cacaattaca ctgccacata 240 tccctagctg agggcagcag taaaatccag gcccgaatgg aacagcagcc cactcgtcct 300 ccacagacgt cacagccacc accacctcca ccacctatgc cattcagagc tccaacgaag 360 cetecagttg gacccaaaac ttetecettg aaagataacc cgtcacetga aceteagttg 420 gatgacatca aaagagagct gagggctgaa gttgacatta ttgaacaaat gagcagcagc 480 agtgggagca gctcttcaga ctctgagagc tcttcgggaa gtgatgacga tagctccagc 540 agtggaggsg aggamaatgg cccagcytct cytccgcagc yttmacacca gcagccytac 600 aacagtaggc etgeegttgc caatggaace ageeggeeac aaggaageaa ecagytyatg 660 aacaccctca gaaatgactt gcagttgagt gagtytggca gtgacagtga tgactagtgc 720 tggatytttc gaaacctact ttttggtgca caaacatgcc gcaagactga gctactttgg 780 ccgtggagtc cattgcaaga ggaaaatgtt atggatcagt gactgtagta ggagtttgag 840 gctytggaac tctcacatat tcaagtcttt aacttagtgg tgatgggtga aaaaaaaaa 900 aaaaaaaaa aa <210> 184 <211> 167

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                             40
Lys Pro Pro Val Gly Pro Lys Thr Ser Pro Leu Lys Asp Asn Pro Ser
                         55
Pro Glu Pro Gln Leu Asp Asp Ile Lys Arg Glu Leu Arg Ala Glu Val
Asp Ile Ile Glu Gln Met Ser Ser Ser Ser Gly Ser Ser Ser Asp
                                    90
Ser Glu Ser Ser Ser Gly Ser Asp Asp Ser Ser Ser Ser Gly Gly
            100
Glu Xaa Asn Gly Pro Ala Ser Xaa Pro Gln Xaa Xaa His Gln Gln Pro
                            120
Tyr Asn Ser Arg Pro Ala Val Ala Asn Gly Thr Ser Arg Pro Gln Gly
    130
                        135
Ser Asn Gln Xaa Met Asn Thr Leu Arg Asn Asp Leu Gln Leu Ser Glu
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Xaa Gly Ser Asp Ser Asp Asp
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325

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965

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35 40 45

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Applicant's or agent's file reference 1290.1001010

International application No.

PCT/US 00/25135

INDICATIONS RELATING TO DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13bis)

·	
A. The indications made below relate to the deposited microorga on pages 335 , line 35	nism or other biological material referred to in the description
B. IDENTIFICATION OF DEPOSIT	Further deposits are identified on an additional sheet
Name of depositary institution	
AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and countercan Type Culture Collection (ATCO 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit	Accession Number
see Attachment A	see Attachment A
C. ADDITIONAL INDICATIONS (leave blank if not applicable	(e) This information is continued on an additional sheet X
of the mention of the grant of a European pater application is refused or withdrawn or deemed deposited with the American Type Culture Col D. DESIGNATED STATES FOR WHICH INDICATIONS AND ADDITIONS ADDITIONS AND ADDITIONS	to be withdrawn, the biological material lection under Accession No. see Attachment A
E. SEPARATE FURNISHING OF INDICATIONS (leave blan	k if not applicable)
The indications listed below will be submitted to the International B Number of Deposit")	tureau later (specify the general nature of the indications e.g., "Accession
For receiving Office use only	For International Bureau use only
This sheet was received with the international application	This sheet was received by the International Bureau on:
Authorized officer Bhalie	Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM (Additi nal Sheet)

C. ADDITIONAL INDICATIONS (Continued)

shall be made available as provided in Rule 28(3) EPC only by the issue of a sample to an expert nominated by the requester (Rule 28(4) EPC).

In respect of the designation of Australia in the subject PCT application, and in accordance with Regulation 3.25(3) of the Australian Patents Regulations, the Applicant hereby gives notice that the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. Affachementa shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention and who is nominated in a request for the furnishing of a sample.

In respect of the designation of Canada in the subject PCT application, the Applicant hereby informs the International Bureau that the Applicant wishes that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. *Aftachment A and referred to in the application to an independent expert nominated by the Commissioner.

Attachment A

-1-

Deposit of Clones

Clones AX65_22, BD335_14, BG241_1, BL187_4, BL249_18, BO71_1, BO365_2, BV51_1, BV140_3, BV141_2, CC194_4, and DA136_11 were deposited on October 3, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

Clones AR415_4, AS63_29, BG160_1, BO432_4, BO538_2, BR595_4, CI490_2, CI522_1, CN238_1, CO390_1, and AY304_1 (an additional isolate of clone AY304_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising a particular polynucleotide is obtainable. Clone AY304_14 wasdeposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20_2, AR440_1, AS164_1, AX8_1, BD176_3, BD339_1, BD427_1, BL229_22, BV123_16, and CH377_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441_1, BD441_2, BG102_3, BK158_1, BP163_1, BZ16_3, CC182_1, CG109_1 and CJ397_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795_4, AT340_1, BG132_1, BG219_2, BG366_2, BV172_2, CC247_10, CI480_9, CO722_1, and CT748_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1_1, AQ73_3, BG142_1, BV66_1, BV291_3, CK201_1, CQ331_2, CT550 1, CT585 1 and CT797 3 were deposited on December 13, 1996 with the ATCC

Attachment A

-2-

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107_1, CG300_3, CJ145_1, CJ160_11, CO20_1, CO223_1, CO310_2, CP258_3, CW1155_3 and CZ247_2 were deposited on December 17, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666_1, BN387_3, BQ135_2, CR678_1, CW420_2, CW795_2, CW823_3, DF989_3, DL162_2, DL162_1, and EC172_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

INTERNATIONAL SEARCH REPORT

International Application No
US 00/25135

A. CLASS IPC 7	FICATION OF SUBJECT MATTER C12N15/12 C07K14/47 C12N1/2 A61K38/17	21 C12N5/10	C12Q1/68
According t	o International Patent Classification (IPC) or to both national classifi	cation and IPC	
	SEARCHED		
IPC 7	ocumentation searched (classification system followed by classifica C07 K		
	tion searched other than minimum documentation to the extent that		
	lata base consulted during the international search (name of data base	·	ns used)
EPU-In	ternal, WPI Data, PAJ, BIOSIS, STRA	AND	
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, of the re	levant passages	Relevant to claim No.
X,L	WO 98 17687 A (GENETICS INST) 30 April 1998 (1998-04-30) the document throws doubt on the of the application abstract; claims 20-22 see SEQ ID NO: 8 and 9 (pp.73-77 page 18, line 30 -page 20, line page 23, line 12 -page 24, line page 31, line 12 -page 64, line) 2 14	1-11
Furth	er documents are listed in the continuation of box C.	X Patent family members are	listed in annex.
*Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *E* earlier document but published on or after the international filing date *E* earlier document but published on or after the international filing date *C* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *C* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document is combined with one or more other such document; such combination being obvious to a person skilled in the art. *C* document member of the same patent family Date of the actual completion of the international search report		ct with the application but e or theory underlying the e; the claimed invention cannot be considered to the document is taken atone e; the claimed invention e an inventive step when the e or more other such docu- obvious to a person skilled patent family	
	December 2000	.3 O. O1, Of	
Hand all III	European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Oderwald, H	

INTERNATIONAL SEARCH REPORT

national application No. PCT/US 00/25135

B x I Obs rvations wh r certain claims wer found unsearchable (C ntinuation of item 1 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
A. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11

An isolated polynucleotide comprising SEQ ID NO: 41 which encodes a protein of SEQ ID NO: 42 (BG160_1). A host cell, a process for producing said protein, a protein produced by said process, a composition comprising said protein.

2. Claims: 12, 13

An isolated polynucleotide comprising SEQ ID NO: 129. A protein encoded by said polynucleotide having amico acid sequence SEQ ID NO: 130 (CO722_1).

nformation on patent family members

International Application No F US 00/25135

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9817687 A	30-04-1998	AU 5004097 A EP 0960199 A	15-05-1998 01-12-1999